

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1566	100.0	300	15	US-10-041-018-46	Sequence 46, Appl
2	1550	99.0	304	9	US-09-925-302-614	Sequence 614, App
3	1550	99.0	304	10	US-09-925-302-614	Sequence 614, App
4	928	59.3	338	15	US-10-041-018-24	Sequence 24, Appl
5	928	59.3	338	15	US-10-041-018-77	Sequence 77, Appl
6	862.5	55.1	335	15	US-10-041-018-23	Sequence 23, Appl
7	862.5	55.1	335	15	US-10-041-018-76	Sequence 76, Appl
8	806.5	51.5	303	15	US-10-041-018-34	Sequence 34, Appl
9	797.5	50.9	428	15	US-10-369-493-4221	Sequence 4221, Ap
10	792	50.6	348	15	US-10-369-493-12405	Sequence 12405, A
11	725	46.3	452	15	US-10-369-493-12982	Sequence 12982, A
12	707	45.1	376	15	US-10-001-192A-15	Sequence 15, Appl
13	613.5	39.2	319	15	US-10-369-493-12991	Sequence 12991, A

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1566	100.0	300	1	GGPP_HUMAN	O95749 h geranylge	
2	1558	99.5	300	2	Q6NW19	Q6nw19 homo sapien	
3	1516	96.8	294	1	GGPP_BOVIN	P56966 b geranylge	
4	1490	95.1	300	2	Q6F596	Q6f596 rattus norv	
5	1476	94.3	300	1	GGPP_MOUSE	Q9wtn0 m geranylge	
6	1322	84.4	327	2	Q7ZTY0	Q7zty0 brachydanio	
7	1163	74.3	236	2	Q9CZZ6	Q9czz6 mus musculu	
8	928	59.3	338	2	O61539	O61539 drosophila	
9	928	59.3	338	2	Q9VS54	Q9vs54 drosophila	
10	888	56.7	357	2	Q7QII9	Q7qii9 anopheles g	
11	862.5	55.1	335	2	O61538	O61538 drosophila	
12	819	52.3	335	2	Q86F69	Q86f69 schistosoma	
13	806.5	51.5	303	2	Q9P885	Q9p885 mucor circi	
14	802	51.2	340	2	Q672V6	Q672v6 aspergillus	
15	797.5	50.9	428	1	GGPP_NEUCR	P24322 n geranylge	
16	794.5	50.7	396	2	Q874I1	Q874i1 emericella	
17	794	50.7	375	2	Q9C452	Q9c452 penicillium	

Database :       A\_Geneseq\_16Dec04:\*  
               1:  geneseqp1980s:\*  
               2:  geneseqp1990s:\*  
               3:  geneseqp2000s:\*  
               4:  geneseqp2001s:\*  
               5:  geneseqp2002s:\*  
               6:  geneseqp2003as:\*  
               7:  geneseqp2003bs:\*  
               8:  geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1566	100.0	300	3	AAy68909	Aay68909 A geranyl
2	1566	100.0	300	8	ADJ10383	Adj10383 Human ger
3	1566	100.0	300	8	ADM98626	Adm98626 Geranylge
4	1550	99.0	304	3	AAB58276	Aab58276 Lung canc
5	1523	97.3	300	2	AAW59753	Aaw59753 Human ger
6	1523	97.3	300	2	AAy27005	Aay27005 Human ger
7	1519	97.0	300	2	AAR97565	Aar97565 Human ger
8	1244.5	79.5	320	4	AAU30743	Aau30743 Novel hum
9	928	59.3	338	4	ABB60947	Abb60947 Drosophil
10	928	59.3	338	8	ADM98657	Adm98657 Geranylge
11	928	59.3	338	8	ADM98604	Adm98604 Geranylge
12	862.5	55.1	335	8	ADM98656	Adm98656 Geranylge
13	862.5	55.1	335	8	ADM98603	Adm98603 Geranylge

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1523	97.3	300	1	US-08-469-665-2	Sequence 2, Appli
2	1523	97.3	300	2	US-09-038-596-2	Sequence 2, Appli
3	1523	97.3	300	5	PCT-US95-00421-2	Sequence 2, Appli
4	707	45.1	376	3	US-09-091-725-15	Sequence 15, Appl
5	583	37.2	335	2	US-08-761-344-2	Sequence 2, Appli
6	238.5	15.2	341	4	US-09-252-991A-21448	Sequence 21448, A
7	229.5	14.7	340	4	US-09-543-681A-5778	Sequence 5778, Ap
8	225.5	14.4	162	4	US-09-248-796A-17986	Sequence 17986, A
9	213.5	13.6	165	4	US-09-248-796A-17985	Sequence 17985, A
10	207	13.2	330	1	US-08-410-167A-4	Sequence 4, Appli
11	207	13.2	330	2	US-08-898-560-1	Sequence 1, Appli
12	206	13.2	330	3	US-09-101-126-1	Sequence 1, Appli
13	197.5	12.6	342	4	US-09-489-039A-13653	Sequence 13653, A
14	197	12.6	353	4	US-09-328-352-4226	Sequence 4226, Ap